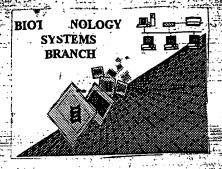
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/674, 237Source: PU/09Date Processed by STIC: 1/11/2001

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE

APPLICANT, WITH A NOTICE TO COMPLY or,

TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/674, 237

ATTN:	NEW RULES CASES: PL	LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
		and a sea of each line "transport" down to the next line
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.
		This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
		The rules require that a line not exceed 72 characters in length. This includes spaces.
3	Incorrect Line Length	The rules require that a line not exceed 72 oriotoxics in rangement and a line not exc
	·	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
4	Misaligned Amino Acid	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
	Numbering	between the numbering. It is recommended to detect any transfer and the period of the
_	Non'ACCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
³ —	Non-ASCII	Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
		Please elistic your subsequent obstances
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.
۰	Variable Length	As per the rules, each n or Xaa can only represent a single residue.
	-	Please present the maximum number of each residue having variable length and
		indicate in the (ix) feature section that some may be missing.
-	Detections 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
′ —	Patentin ver. 2.0 "bug"	sequence(s) Normally, Patentin would automatically generate this section from the
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
		Sections for Artificial of Official Sections 101
	Oliver d Commence	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
8	Skipped Sequences	12) INFORMATION FOR SEO ID NO:X:
	(OLD RULES)	(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
		This sequence is intermonally suppose
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
		(-
0	Skinned Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
9	Skipped Sequences	<210> sequence id number
1	(NEW RULES)	\$400> sequence id number
- 1		000
1		
10 V	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.
10		
	(NEW RULES)	In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
		(II C220) to C220, Section, product expression and
	ttee of cotto Connectors	Sequence(s) are missing this mandatory field or its response.
11	Use of <213>Organism	Sequence(s) are missing the
	(NEW RULES)	
40	Line of s220s Feeture	Sequence(s) are missing the <220>Feature and associated headings.
12	Use of <220>Feature	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
	(NEW RULES)	Please explain source of genetic material in <220> to <223> section.
	•	(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules
		(See Federal Register, Old 1190, Vol. 00, 110. 101, pp. 20001 02)
		#Gt- Distriction of Patentle version 2.0. This causes a corrupted
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted
	Dimension of	Tite, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
		Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING

DATE: 01/11/2001 TIME: 17:14:19

PATENT APPLICATION: US/09/674,237

19/0/4,23/ 11888. 17.14.3

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Output Set: N:\CRF3\01112001\1674237.raw

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3 <110> APPLICANT: HSC RESEARCH AND DEVELOPMENT LIMITED PARTNERSHIP
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5 <120> TITLE OF INVENTION: ESE GENES AND PROTEINS

7 <130> FILE REFERENCE: 3206-169/PAR

9 <140> CURRENT APPLICATION NUMBER: US/09/674,237

10 <141> CURRENT FILING DATE: 2000-10-27

12 <150> PRIOR APPLICATION NUMBER: 2,230,201

13 <151> PRIOR FILING DATE: 1998-04-27

15 <160> NUMBER OF SEQ ID NOS: 33

17 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

512 <210> SEQ ID NO: 3 513 <211> LENGTH: 1213 514 <212> TYPE: PRT 515 <213> ORGANISM: Mus musculus 517 <400> SEQUENCE: 3 518 Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala 519 1 5 10 15 519 1 5 521 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu 522 20 25 524 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe 525 35 40 45 527 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu 528 50 55 60 530 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile 531 65 70 75 80 533 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser 534 85 90 95 536 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala 537 100 105 110 539 Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala 540 115 120 125 542 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro 543 130 135 140 545 Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn 546 145 150 150 160 548 Gly Ala Pro Pro Val Ile Glm Pro Leu Pro Ala Phe Ala His Pro Ala 165 170 551 Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser 552 180 185 190 554 Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser 555 195 200 205 557 Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys 220 215 558 210 560 Tyr Arg Cln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu



DATE: 01/11/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/674,237 TIME: 17:14:19

561	225					230					235		_			240
563	Thr	Gly	Pro	Gln	Ala	Arg	Thr	Ile	Leu	Met	G1n	ser	Ser	Leu	Pro	GIn
564					245					250					255	
566	Ala	Gl n	Leu	Ala	ser	11c	тrр	Asn		Ser	Asp	I l.e	Asp	GIn	Asp	GIY
567				260					265					270		
569	Lys	Leu	Thr	Ala	Glu	Glu	Phe	Lle	Leu	Al.a	Met	His	Leu	rle	Asp	Val
570			275					580					285			
572	Ala	Met	Ser	Gly	Gln	Pro	ren	Pro	Pro	Val	Leu	Pro	Pro	Glu	Tyr	rle
573		290					295					300				
575	Pro	Pro	ser	Phe	Arg	Arg	Val	Arg	ser	Gly	ser	Gly	Met	ser	Va l.	Tle
576	305					310					315					320
578	Ser	Ser	Ser	Ser	Val	Asp	Gln	Arg	Leu	Pro	Glu	Glu	Pro	Ser	Ser	Glu
579					325					330					335	
583	Asp	Glu	G.Ln	G1.n	Pro	Glu	Lys	Lys	Leu	Pro	val	Thr	Phe	GLu	Asp	Lys
582				340					345					350		
584	LVS	Arg	Glu	Asn	Phe	Glu	Arg	Gly	Ser	Val	Glu	Leu	Glu	Lys	Arg	Arg
585	•	,	355					360					365			
587	Gln	Ala	Leu	Leu	Glu	Cln	G.l.n	Arg	Lys	Glu	Gln	Glu	Arg	Leu	Ala	Gln
588		370					375					380				
590	Leu	Glu	Arq	Ala	Glu	Gln	Glu	Arg	Lys	Glu	Arg	Glu	Arg	Gln	Glu	Gln
591	385					390					395					400
593	Glu	Ala	Lys	Arg	GIn	Leu	Glu	Leu	Glu	Lys	Gl.n	Leu	Glu	Lys	Gln	Arg
594					405					410					415	
596	Glu	Leu	Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	11e	Glu	Arg
597				420		_			425					430		
599	Arq	Glu	Ala	Ala	Lys	Arg	Glu	Leu	Glu	Arg	Gln	Arg	Gln	Leu	Glu	Trp
600			435					440					445			
602	Glu	Arg	Asn	A.rq	Arq	Gln	Glu	Leu	Leu	Asn	Gln	Arg	Asn	Lys	Glu	Gln
603		450		-	-		455					460				
605	Glu	Glv	Thr	Val.	Val	Leu	Lys	Ala	Arg	Arg	Lys	Thr	Leu	Glu	Phe	Glu
606	465					470					475					480
608	Leu	Glu	Ala	Leu	Asn	Asp	Lys	Lys	His	Gln	Leu	Glu	Gly	Lys	Leu	Gln
609					485					490					495	
611	Asp	He	Arg	Cys	Arg	Leu	Ala	Thr	Gln	Arg	Gln	GLu	Ile	GLu	Ser	Thr
612				500					505					510		
614	Asn	Lys	Ser	Arg	Glu	Leu	Arg	Tle	Ala	Glu	T-l.e	Thr	Hi.s	Leu	Gln	Gln
615			515					520					525			
617	Gln	Leu	Gln	Glu	ser	Gln	$_{ m Gln}$	Met.	Leu	Gly	Arg	Leu	$_{\rm Ile}$	Pro	Glu	Lys
618		530					535					540				
620	Gln	Tle	Leu	Ser	Asp	Cln	Leu	Lys	Gln	Val.	Gln	Gln	Asn	Ser	Leu	His
621	545					550					555					560
623	Arg	Asp	ser	Leu	Leu	Ťhr	Leu	Lys	Arg	Ala	Leu	Glu	Ala	Lys	Glu	Leu
624					565					570				•	575	
626	Λla	Arg	Gln	Gln	Leu	Arg	GLu	Gln	Leu	Asp	Glu	Val	Glu	Arg	Glu	Thx
627				580					585					590		
629	Arg	Ser	Lys	Leu	Gln	Glu	Ile	Asp	Val	Phe	Asn	Asn	Gln	Leu	Lys	Glu
630			595					600					605			
632	Leu	Arg	G1 u	Ile	His	ser	Lys	Gln	Gln	Leu	Gl n	Lys	Gln	Arg	Ser	Leu
633		610					615					620				

DATE: 01/11/2001 TIME: 17:14:19

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/674,237

	Glu 625	Ala	Ala	Arg	Leu	Lys 630	Gln	Lys	Glu	Gln	Glu 635	Arg	Lys	Ser	Leu	Glu 640
		Glu	Lvs	Gln	Lys	Glu	Asp	Ala	Gln	Arq		Val	Gln	Gl.u	Arg	
639			•		645		•			650					655	
	Lys	Cln	Trp			His	Val	Gln		Glu	Glu	Gln	Pro		Pro	Arg
642	T	**	T) 4	660				7 4	665	7	C1) an	Can	670	٨٠٠	Lua
645	rys	ЬLО	675	Giu	GLU	Asp	arg	680	ràs	ALG	GIU	ASD	685	val	Arq	ьys
	LVS	Glu	-	Glu	Glu	Arq	Ala		Pro	GLu	Met	Gln		Lys	Gln	Ser
648	•	690					695	-				700	•			
650	Arg	Leu	Phe	His	Pro	His	Gln	Glu	Pro	Ala	-	Leu	Ala	Thr	Gln	
	705			_		710			_	_	715		_			720
	Pro	Trp	Ser	Th.r	725	Glu	ГÄЗ	Gly	Pro	Leu 730	Thr	He	ser	ALa	GIn 735	GLu
654 656	Cor	Wal	Tave	Va I		Tyr	Twr	Δra	Δla		m. r	Pro	Phe	Gln		Λrα
657	JUL	Y U.L.	шуз	740	Vul	L 1 L	1/1	211 9	745	БСи	- 1 -	110	2110	750	001	11119
659	ser	His	Asp	Glu	Ile	Thr	Ile	${\tt Gln}$	Pro	Gly	Asp	Ile	Val	Met	Val	Asp
660			755					760					765			
	Glu		Gln	Thr	Gly	Glu		Gl y	Trp	Leu	Gly		Glu	Leu	Lys	Gly
663	1	770	Cl.	(flace)	nho	Dasco	775	7 cm	Mar er	712	Clu	780	Tlo	Dro	Clu	Aen
666	785	THE	GTĀ	ттр	PHE	Pro 790	Ald	ASII	туг	AJ. a	795	цув	1.16	PTO	GIU	800
		Val	Pro	Thr	Pro	Ala	Lys	Pro	Va1	Thr		Leu	Thr	Ser	Ala	
669			,		805					810	•				815	
	Ala	Pro	Lys		Ala	Leu	Arg	Glu		Pro	Ala	Pro	Leu		Val	Thr
672		_		820			mil		825	•		~	•	830	a	a
674	ser	Ser	835	Pro	ser	Thr	Tur	840	ASII	Asn	тгр	Ата	845	Phe	ser	ser
	Thr	Trp		ser	ser	Ser	Asn		Lvs	Pro	Glu	Thr	-	Asn	Trp	Asp
678		850					855					860				
680	Thr	Trp	Ala	Ala	Gln	Pro	Ser	Leu	Thr	Va l	Pro	ser	A.l.a	Gly	Gln	Leu
681	865					870					875			_		880
683 684	Arg	GLn	Arg	Ser	885	Phe	Thr	Pro	Ala	Thr 890	Ala	Thr	GIY	Ser	ser 895	Pro
	Ser	Pro	Val	Len		Gln	Glv	Glu	Lvs		Glu	Glv	Leu	Gln		Gln
687	DCL	110	1 4 1.	900	O L j	01.11	0.2.1	0	905	,	0	0.1	200.1	910		0
689	Ala	Leu	Tyr	Pro	Trp	Arg	Ala	Lys	Lys	Asp	Asn	His	Leu	Asn	Phe	Asn
690			915					920					925			
	Lys		Asp	Val.	Tle	Thr		Leu	Glu	Gln	Gln	_	меt	Trp	Trp	Phe
693	C111	930	Ma l	cln	Clu	Gln	935	Clu	Пrn	Dho	Dro	940	Cor	Diver	V = 1	Tvo
696	945	G.Lu	va 1	GTII	Gry	950	LlyS	GLy	ттр	FRE	955	ыуы	Ser	ту і.	Vai	960
		Ile	Ser	Gly	Pro	Val	Arg	Lys	ser	Thr	-	Ile	Asp	Thr	Gly	
699				-	965		_	-		970			-		975	
	Thr	Glu	ser		Ala	Ser	Leu	Lys		Val	Ala	ser	Pro		Ala	Lys
702	Dans	2.1 -	r1-	980	01	<i>0</i> 1	C1.	nh =	985	43-	Mat	(Dec.	mb	990	'clv	Cor
704	Pro	Ala	11e	PFO	GTA	Glu		Pne L000	116	ATG	мес	-	unii 1005	туг	GIU	Ser
	Ser	Glu		Gly	Asp	Leu			Gln	Gl.n	Gly	-		He	Val	Va l.
			-	-	1.	_	•	_	-	_	-	-				

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/674,237

DATE: 01/11/2001 TIME: 17:14:19

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Output Set: N:\CRF3\01112001\1674237.raw

1015 708 1010 1050 1045 716 Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys Pro Glu Ile Ala 717 1060 1065 1070 719 Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro Glu Gln Leu Thr Leu 720 $$ 1075 $$ 1080 $$ 1085 722 Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp 1100 723 1090 1095 725 Trp Glu Gly Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp E--> 726 105 1110 1115 1120 728 Phe Pro Ala Asn Tyr Val Lys Leu Leu Ser Pro Gly Thr Ser Lys Ile 1125 1130 729 731 Thr Pro Thr Glu Leu Pro Lys Thr Ala Val Gln Pro Ala Val Cys Gln 732 1140 1145 1150 734 Val Ile Gly Met Tyr Asp Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala 735 1155 1160 1165 735 1155 1160 737 Phe Ser Lys Gly Gln Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp 738 1170 1175 1180 738 1170 740 Trp Trp Lys Gly Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn
E--> 741 185 1190 1195 1200
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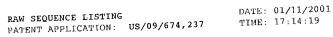
1255 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro

When humbering first anero acid on a line, begin the number when the first letter of the americ acid. Please leave a space between exterie number and next americ acid.

DATE: 01/11/2001 TIME: 17:14:19

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/674,237

				-												160
1256 1	15					150					155	_	_	.	т1	
1256 1: 1258 Se	יזר. איזר	/al	ser	Thr	Ser	ser	Leu	Pro	Asn	Cly	Thr	Ala	Ser.	Leu	110	G111
1259 1261 Pi	ro I	l.eu	ser	Ile	Pro	Tyr	ser	ser	ser	Th r	ren	Pro	H1.S	ALa	ser	Ser
1262 1264 T	vr :	Ser	Leu	Met	Met	Gly	GLY	Phc	GLY	Cly	Ala	Ser	116	Gin	Lys	ALG
1265 1267 G	ln :	Ser	Leu	Tle	Asp	Leu	Gly	ser	Ser	Ser	Ser	Thr	ser	ser	THL	ATO
1268 1270 S	er	Leu	Ser	Gly	Asn	ser	Pro	Lys	Thr	Cly	Thr	ser	GLu	rrp	ALG	210
1271 2 1273 P	ro	G].n	Pro	Ser	Arg	Leu	Lys	туr	Arg	Gln	Lys	Phe	Asn	Ser	255	дар
1274 1276 L	7S	Gly	Met	Ser	Gly	Tyr	Leu	ser	Gly	Phe	GIn	Ala	Arg	220	Ara	11011
1277 1279 L	.eu	Gln'	ser	Asn	Leu	ser	Gln	T'hT	G L ti	Leu	Ala	Thr	285	TLP	1111	ден
1280 1282 A	La	Asp	Ile	Asp	Gly	Asp	Gly	Gln	Leu	Lys	Ala	300	GTU	PHE	110	DC.
1283 1285 A	la	Met	His	Leu	Thr	Asp	Met	Ala	Lys	Ala	CTA	GTH	10	LiC. a	1 2 0	320
1286 3 1288 1	hr	Leu	P.ro	Pro	Glu	Leu	Val	Pro	Pro	Ser	PHE	mig	Gry	Q.c.j	335	
1289 1291 \	/al	Asp	ser	Val	Asn	Gly	Thr	Leu	Pro	ser	171	(3.1.11	шуо	350	0	
1292 1294 (31.u	Glu	Pro	Gln	Lys	Lys	Leu	360	va i	1111	FIIC	() 1.14	365		-	_
1295			355			0.1 -	2	300 Mot	c Lu	Len	Glu	LVS			Glr	Val.
1295 1297 <i>I</i>	Al.a		Tyr	Glu	Arg	GIY	ASI	Mec	GIU	. 1100	01	380				
1298 1300 I		370			a1.	C2 n	375	Clu	Δla	Gle	ı Ara	Lvs	Ala	Gln	Lys	Glu
1301 1303	385		a 1	(T) =0 =0		370	T.vre	Gln	Arc	Glu	ı Leu	Gln	GLu	Glr	Glu	Trp
1304 1306		Ŧ =	C I n	. Tou	Clu	Len	Glu	LVS	Arc	Let	ıGlu	Lys	Glr	Are	g Glu	ı Leu
1307 1309	<i>a</i> 3	A 20/1	Clr	92C	r Gli	Glu	Glu	Arc	Arc	Lys	s Glu	ı Tle	Glu	ı Arç	, Ar	g Glu
$\frac{1310}{1312}$	2.1.5	۸ J ص	177	, Glr	a Gli	Leu	Glu	Arc	Gli	Ar	j Arg	, Lei	ı Glu	ı Tr	o Gli	ı Arg
1313 1315	Lou	7.7C	. Arc	r Glr	n Glu	Let	Leu	se:	c G1:	a Ly	s Thi	c Arg	g Gli	ı Glı	a Gl	ı Asp
$\frac{1316}{1318}$	T10	Val	Δro	ı Lei	ı sei	sei	: Ar	Ly:	s Ly:	s Se.	r Lei	ı His	s Let	ı Glı	ı Le	ı Glu
1319 1321	Δla	Val	Ası	n GI	y Ly:	s His	s Gli	a Gla	n Il	e Se	r Gl	y A.r.	g Lei	u Gl	n As	p var
1322 1324	Gln	T 1 e	a Are	q Lv:	s Gl	n Thi	c Gla	а Бу	s Th	r Gl	u Le	u Gl	u Vai	ı Le	u As	ь гаг
1327	Gln	Cys	s As	р Le	u Gl	u Ile	e We	t Gl	u Il	e Ly	s Cl	n Le	u G1	n Gi	пет	u Leu
1328		530					53	5				54	U			
1000																



			t pu t				(
1330 Lys C	m	C	ln A	en 1.	vs I	eu	11e	Tyr	Leu	Val	Pro	Glu	Lys	Gln	Leu	
1330 Lys G	ilu T	yı. G.	1,11 25.	5 5	50			-		555					560	
1331 545 1333 Leu A	an C	ln Δ	ra T	le L	vs 7	Asn	иet	Gln	Leu	ser	Asn	Thr	Pro	Asp	ser	
1333 Leu /	ISH G	1u n	+9 ·	65	7				570					575		
1334 1336 Gly 1	r1 / C	or L	eu T	en E	is	Lys	Lys	ser	ser	Glu	Lys	Glu	GLu	Leu	Cys	
1336 GIY 1	rite 9	er n	80			4	-	585					590			
1337 1339 Gln /	T	ا بدہ	ve C	1n 6	:In	Leu	ASD	Ala	Leu	G l.u	Lys	Glu	Thr	Alla	ser	
1339 Gin A	4.F9 L	95	iy 5 G	, <u>, , , , , , , , , , , , , , , , , , </u>			600					605				
1340 1342 Lys L		95 000 C	la M	ust A	450	ser	Phe	Asn	Asn	Gln	Leu	ΓÄS	Glu	Leu	Arg	
1342 Lys	Leu S	er o	11.11 1	icc .	T. F	615					620					
1343 1345 Glu	0 T O	1	en T	hr (aln	Gln	Leu	Ala	Let	Glu	Gln	Let	His	Lys	ITG	
1345 GLu	ser 1	YY Z	1211 1	.111. 1	530	G.2.				635	,				640	
1346 625 1348 Lys			*** T	OII I	LVS	Glu	ile	Glu	Arg	Lys	Arg	Let	ı Gli	Gln	Tle	
1348 Lys	Arg F	sp i	ys t	545	11.				650)				655		
1349 1351 Gln				. 011 1	210	Asn	Glu	Ala	Ala	Arg	Lys	Ala	ı Lys	Glr	Gly	
1351 Gln	Lys I	.γs i	.ys 1	beu .	J J. U	. no p		665					670)		
1352 1354 Lys		1	000	D acres	A rea	Glu	Ser	Ile	Ar	J Lys	s Glu	Gl	ıGlı	ı Glu	LYS	
1354 Lys	Glu A	ASB J	цеп .	irb.	arg	OLG	680					68	5			
1355 1357 Gln	_	0/5	/	a I n	c Lu	G1 o	LVS	ser	G1.	n Ası	o Lys	Th:	r Gl	a Glu	ı Glu	
1357 Gln	Lys	Arg .	ьен ч	1,1,11	(7,1.11	695	27.0				700)				
1358 1360 Glu	690		. 1	C111	Λla	LVS	Glo	Ser	G1	u Th	r Ala	ı se	r Al	a Le	ı Val	
1360 Glu	Arg	Lys	Ala '	GΙU	710	шуо	0			71	5				720	
1361 705 1363 Asn			. 1 .	T 011	U.T.L.	Dro	Phe	Gli	ı Al.	a Ar	g Ası	n Hi	s As	p Gl	ı Met	
1363 Asn	Tyr.	Arg	ALd	725	1 7 1	1.10	,		73	0				73	5	
1364 1366 ser			a	723	Acn	Tle	116	e Gla	. Va	l As	p Gli	a Ly	s Th	r Va	1. G1.y	1
1366 Ser	Phe	ser	ser	GTA	HSP	.110	, ,,,,,,	74	5		-		75	0		
1367 1369 Glu		- ·	740	T	Therm	c:1s	, Se1	Phe	e G1	n Gl	у Ьу	s Ph	e Gl	y Tr	p Ph€	3
1369 Glu	Pro	GIA	arp	neu	1 7 1	Gir	760)				76	5			
1370 1372 Pro		755	FF1	17m 1	clu	T.375	. Va	Le	n Se	r Se	r Gl	u Ly	s Al	a Le	u Sei	C
1372 Pro	Cys	Asn	TÄL	Val	GTU	775	, ,				78	O)				
1373 1375 Pro	770		3 1 5	f ou	Tou	pro	n Pro	o Th	r Va	ıl se	r Le	u Se	r Al	a Th	r Sei	r
1375 Pro	Lys	ràs	Ald	Leu	790	120				79	5				80	ð
1376 785 1378 Thr		_	a1	Dec	Dec	. 7.1:	a Se	r Va	1 Ti	ır As	р Ту	r Hi	s As	n Va	1. Se:	r
1378 Thr	ser	ser	GIH	805	PIC	, LI	u oc.		8:	LO	•			81	.5	
1379 1381 Phe				002	57-5 1	٨٥	n Th	r Th	r T	cp Gl	n Gl	n Ly	s Se	er Al	a Ph	e
1381 Phe	Ser	Asn	Leu	THE	Agr	. 11.3		82	5	-			8	30		
1382 1384 Thr		1	820	Com	Dave	. 61	v Se	r Va	1 8	er Pi	co Il	e H	is G	ly Gl	n Gl	У
1384 Thr	Arg	Thr	Val	Ser.	PIC) G.L	84	0				8	45			
1385 1387 Gln		835	a3	3.00	т от	. T 12	e A1	a Gl	n ·A	la Le	eu Cy	s S	er T	rp Ti	ır Al	a
1387 Gln	Ala	Val	GLU	ASII	Tie: (85	5				86	0				
1388 1390 Lys	850				T 0.	. 70	n Dh	6 56	r T	vs H	is As	sp V	al. T	le T	ar Va	1
1390 Буя	Lys	GLu	ASN	HLS	874	ı AS	41 E 11		- ,	8	75				88	0
1391 865 1393 Lev	5			0.1	0/1	n mar	n Tr	n pl	ne G	lv G	lu Va	al H	is G	ly G	ly Ar	:ġ
1393 Leu	ı Glu	GIn	GIN	GTR	AS	11 11	P 11	E,	8	90				8	95	
1394 1396 Gly			_	885		v m∗	r V=	a to	zs T	eu I	le P	ro G	ly A	sn G	Lu Va	:1
1396 Gl	Trp	Phe	Pro	гÀа	5 50	1 17	J. V.C	زند بد، ۱۹	,5 t. 05				9	10		
1397 1399 Gli		"	900	D	1	1	a 14	ייף זוב	or A	la A	la V	al T	hr L	ys L	ys Pi	CO
1399 Gl:	n Arg	Gly	Glu	Pro	ביט נ	u Hl	ימ דופ	20	,			9	25			
1400 1402 Th		91.5		m.	. D	a V	יע ויח די	nr S	er 1	hr A	la T	yr E	ro V	al G	1y G:	l.u
1402 Th.	r ser	Thr	Ala	t d.A.	PI	U V	3.L J. J	٠.١. ١.١	·		-	-				

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       1411 Trp Trp Thr Gly Ser Ile Gly Clu Arg Thr Gly 11e Phe Pro Ser Asn 1412 980 985 990
       1414 Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
1415 995 1000 1005
1415 995 1000 1005

1417 Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala Tyr

1418 1010 1015 1020

1420 Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln Leu Ile

1421 1025 1030 1035 1040

E--> 1422 025 1030 1035 1040

1423 Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly Glu Leu Gln

1424 1045 1045 1050 1055
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       1429 Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala
1430 1075 1080 1085
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1435 Gly Leu Asn Phe Ser Lys Gly Gln Leu Ile Asn Val Met Asn Lys Asp
E--> 1436 105 1110 1115 1120
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        1441 Pro Ser Asn Tyr Val Lys Met Thr Thr Asp Ser Asp Pro Ser Gln Gln 1442 1140 1145 1150
        1444 Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg
1445 1155 1160 1165
        1447 Lys Arg Gln Gly Tyr Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr 1448 1170 1175 1180
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         2753 <213> ORGANISM: Mus musculus
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         2759 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu 2760 20 25 30
         2762 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe 2763 \phantom{-}35\phantom{+}40\phantom{+}45\phantom{+}
         2765 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
2766 50 55 60
         2768 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
2769 65 70 75 80
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2771 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser

same eno



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										0.0					95	
2772					85				*	90	17- 1	3.1.5	т 1 го	car		Ala
$\frac{2772}{2774}$	Thr	Leu	Pro	Pro	۷al ·	Met	Ŀуs	Gln	G.l.n	Pro	Val	Ald	LIC	110	JC.	
				100					11117					F. 30. 0		
2775 2777	Pro	Ala	Phe	Gly	11e	Gly	Gly	He	Ala	ser	Met	PIO	125	Lieu	1111	1124
$\frac{2778}{2780}$	val	Ala	Pro	Val	Pro	Met	GIA	Ser	lle	Pro	Val	Val	GTĀ	MCL	PGI	21.0
2781 2783	Pro	Leu	Val	Ser	ser	Val	Pro	Pro	Ala	Ala	Val	Pro	Pro	ren	Ard	160
$\frac{2784}{2786}$	Glv	Ala	Pro	Pro	Val	Ile	Gln	Pro	Leu	Pro	Ala	Phe	Ala	HIS	PLO	ALG
2787 2789	Ala	Thr	'f'rp	Pro	Lys	Ser	Ser	Ser	Phe	ser	Arg	Ser	Gly	Pro	GLY	ser
2790 2792	Cln	Leu	Asn	Thr	Lys	Leu	Gln	Lys	Ala	Gln	ser	Phe	Asp	Val	Alla	ser
2793 2795	Λla	Dro	Pro	Ala	Ala	Glu	Trp	Ala	Val	Pro	Gln	ser	Ser	Arg	Leu	Lys
2790	Mur	320	Cln	Lon	Phe	Asn	Ser	His	Asp	Lys	Thr	Met	ser	Gly	His	Leu
2/99	mbe	Clu	Dro	Gln	Ala	Ara	Thr	Tle	Leu	Met	Gln	Ser	Ser	Leu	bro	GIn
2802	23.2	cin	Lou	λla	Ser	Tle	Trp	Asn	Leu	ser	Asp	rle	Asp	Gln	Asp	$GJ\lambda$
2805		r	mh x	7.13	c1n	GTu	Phe	Ile	Leu	Ala	Met	His	Leu	lle	Asρ	Val
2808			2/3	C111	Cln	Pro	T.(>1)	Pro	Pro	Val	Leu	P.ro	Pro	Glu	Tyr	ile
2811		290		nho	λκα	7, 200	Val	Ara	Ser	Glv	ser	Gly	Met	ser	Val	11e 320
2814	305				. v-1	yen	(21)	Ara	Leu	Pro	Glu	G1u	Pro	Ser	ser	Glu
2817		a.)		. alm	723	. (31)	1.576	LVS	Leu	Pro	val	Thr	Phe	e Glu	Asp	Lys
2820	}		a 1.	340	nha	Clu	Arr	r Glv	Set	· Val	L GI	Leu	Cli	Lys	Arç	Arg
2823	3	_ ,	355			C'lr	cli) Arc	r T.V.S	s Glu	1 G1:	n Glu	ı Arg	j Lei	Ala	Gln
2826	5	370) • • • •	1 -		. c1r	. Gl	, , Arc	a Tive	s Gla	ı Aro	g Glu	Arg	g Glr	Glu	1 Gln 400
2829	9 385				- 01.	J9(, (1)	LIGI	. 613	i Tiv	s GL	n Leu	ı Gl	и Туя	s Gli	arg 5
		1 A.L	я глу	s Arq	J G.LI	- Tiest	1 (7.1.1	1 1100	. 0.20	41	0			-	413	5
283	2		1	_	405) - 30		o Cli	. (3)	n Ar	a Ar	a Lv:	s C1	u Ile	e Gli	ı Arg
283	5		_	420)	. 7	- 01	u foi	42. 1. (21)	u Ar	a Gl	n Ar	a Gl	n Lei	ı Gl	ı Trp
		g GI:	u Ala	a Ala	я гуя	s Arg	<i>y</i> 6.1	u 1.00	n n	14 11.L	5 01		44	5		ı Trp
284	0 Gl	u Ar	g As	n Ar	g Ar	g 611	I OT	u wel	u ne	u no	01	46	0			u Gln
284	1	45	U .			y .e -	45) a 7,1.	a Ar	a Ar	a Lv	c Th	r Le	u G1:	u Ph	e Glu 480
			y Th	r Va	r va.	r rei	u Ju∑ o	o Al	u Bi	a ur	47	5		- "		480
284	4 46	5				47	U				-1 /	-				

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	Leu	Glu	Ala	Leu	Asn 485	Asp	Lys	Lys	His	Gln 490	ren	Glu	Cly	Lys	Leu 495	Gln
2847	Asp	rle	Ara	Cvs		Len	Ala	Thr	GIn		Gln	Glu	1le	Glu		Thr
2850				500		200			505	,				510		
2852	Asn	Lys	ser	Arg	Glu	Leu	Arg	Ile	Ala	Glu	Ile	Thr	His	Leu	Gln	Gln
2853			515					520					525			
	Gln		Gln	Glu	Ser	Gln		Met	Leu	Gly	Arg		ile	Pr.o	G.l u	Lys
2856		530			_	~ 1	535		0.3	37.3	~1	540			·	0.4
	Gln 545	11.0	Leu	Ser	Asp	550	Leu	Lys	G I.B	va L	555	GIN	ASII	ser	Leu	560
	Arq	Aen	Ser	T.6311	Len		Len	Lvs	Ara	Δla		Clu	Ala	Luc	Glu	
2862			001	2200	565		1100	22,0	9	570	200			2010	575	
2864	Ala	Arg	Gln	Gln	Leu	Arg	Glu	G1n	Leu	Asp	Glu	Va1	G1.u	Arg	Glu	Thr
2865				580					585					590		
	Arq	Ser		Leu	Gln	Glu	Ile		Val	Phe	Asn	Asn		Leu	Lys	Glu
2868			595					600			3	_	605	_	_	_
	Leu		Glu	He	His	Ser		GIn	Gln	Leu	GIn	Lys 620	GIn	Arg	Ser	Leu
2871	Glu	610	7.1.a	W meet	LOU	Tuc	615	Lvc	cto	Cln	Clu		T.37.0	Sar	Lau	<i>a</i> 10
	625	Ald	H.1. a	arg	17671	630	(3.1.11	шуы	G.E.G	0 1.11	635	nrg	uya	O Call	nea	640
	Leu	G l.u	Lvs	Gln	Lys		Asp	Ala	G l.n	Arq		Va1	G1n	Glu	Arg	
2877			-		645					650					655	-
2879	Lys	Gln	Trp	Leu	$_{\rm G.l.u}$	His	Val.	Gl.n	${\tt Gln}$	${\tt Glu}$	Glu	Gln	Pro	Arg	Pro	Arg
2880				660					665					670		
	Lys	Pro		Glu	Glu	Asp	Arg		Lys	Arg	Glu	Asp		Val	Arg	Lys
2883		a 1	675	01	a1	3	7.1.0	680	200	(2.1.)	Mot	C2 5	685	f.ra	Clo	Con
2886	Lys	690	Ald	GIU	Gill	Arg	695	ьуѕ	PLO	G J, U	мес	700	ASP	uγs	GIII	261
	Arq		Phe	His	Pro	His		Glu	Pro	Ala	LVS		Ala	Thr.	Gln	Ala
	705					710					715					720
2891	Pro	Trp	Ser	Thr	Thr	Glu	Lys	Gly	Pro	Leu	Thr	Ile	ser	Ala	Gln	G1u
2892					725					730					735	
	Ser	Val	Lys		Val	Tyr	Tyr	Arg		Leu	Tyr	Pro	Phe		Ser	Arg
2895				740	* 1 -	ml	. 1 -	cz 1	745	01		r1.	57 - 1	750	57 m 1	
2897	Ser	HIS	755	GIU	тте	THE	rre	760	PLO	G.L.Y	Asp	rie	765	Net	val	asp
	Glu	Ser		Thr	Glv	Glu	Pro		Trp	Leu	Glv	Gly		Len	Lvs	Glv
2901		770	01.11		011		775		F			780			-1-	2
2903	Lys	Th.c	Gly	Trp	Phe	Pro	Ala	Asn	туг	Ala	GLu	Lys	Tle	Pro	Glu	Asn
2904	785					790					795					800
	Glu	Val	Pro	Thr		Ala	Lys	Pro	Val		Asp	Leu	Thr	Ser		Pro
2907				_	805			~ 1	mì	81.0				.	815	m) .
2909 2910	Ala	Pro	Lys	Беи 820	Ala	ьеи	arg	GIU	Thr 825	Pro	ALa	Pro	теп	830	vaı	THE
	ser	Ser	Glu		Ser	Thr	Thr	Pro		Agn	Tro	Ala	Asp		Ser	Ser
2913	00.1	JC1.	835		501	2111	1112	840	.150	. 1011	~~ I	, , , , , ,	845		~~.	J C. 1.
	Thr	Trp		Ser	ser	Ser	Asn		Lys	Pro	Glu	Thr		Asn	Trp	Asp
2916		850					855		-			860	-		-	-
291.8	Th.r	T.cp	Ala	Ala	Gln	Pro	Ser	Leu	Thr	Val.	P.ro	Ser	Ala	Gly	Gln	Leu

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	2922			_		885					890			_		895	
	2924	Ser	Pro	Va1	Leu	Glv	Gln	G17	Glu	LVS	Va 1.	G1.u	Glv	Leu	Gln	Ala	Gln
	2925				900	2				905					910		
	2927	Δla	Lou	Tyr		Trn	Ara	Ala	Lve			Agn	His	Leu		phe	Asn
	2928	11.1.0	LC.U	915	1.20	1 1. [2	2325	211.4	920	DIO	2156	11011	11 2.5	925	11011	1110	1 11011
	2930	T 110	cor		Val	Tlo	whr	17 to 1		Clu	Cln	Cln	Aan		(I) rery	Thro	Dho
	2930	uys	930	vah	Val	LLE	III	935	neu	OLG	GIII	GIH	940	Merc	1 1. }/	115	FILE
		G1		1 (m)	01.0	a3	C1		a1	ffi eren	Oho	Dwo		Com	Mr. on	Un T	7
	2933	_	GIU	V d I.	GLII	617		LYS	QT.	rrp	PHE		ьуѕ	261	туг	val	
	2934	-			- 2		950				(0.1	955	· 1		m)		960
	2936	Leu	11.e	ser	GLY		Val	Arg	Lys	ser		ser	rre	Asp	Thr	_	Pro
	2937					965					970					975	•
	2939	Thr	Glu	Ser		Ala	Ser	Leu	Lys		Val	Ala	Ser	Pro		Ala	Lys
	2940				980					985					990		
	2942	Pro	Ala	He	Pro	Gly	Glu	Glu	Phe	Tle	Ala	Met	Tyr	Thr	$ ext{Tyr}$	Glu	Ser
	2943			995					1000					1005			
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	2946	3	1010				3	.015					L020				
	2948	Thr_	Lys	Lys	Asp	Gly	Asp	Trp	Trp	Thr	Gly	Thr	Val	Gly	Asp	Lys	Ser
E>	2948	025	107	25		1	1030					035]	L040
	2951				Pro	Ser	Asn	Tyr	Val	Arq	Leu	Lys	Asp	ser	Glu	Gly	ser
	2952					1045		•			1050	•	-			1055	
	2954	Gly	Thr	Ala	Glv	LVS	Thr	Gly	Ser	Leu	Glv	Lvs	Lvs	Pro	Glu	He	Ala
	2955				1.060	-,, -				1.065		-,-	2		1070		
	2957	Gln	Val			Ser	Tyr	Ala			Glv	Pro	Glu			Thr	Len
	2958	0 1.11		1075		D1.24.	- 1 -		080	2	U 1			1085		1 1133	Dou
	2960	Δla			Gln	Lon	TIA			Ara	Lve	Tare			G3 v	Gly	Trn
	2961		090	GLy	GIN	11C (1		.095	.1 1.0	1119	LIYS	-	1100	1 1.0	G.E.	OLy	115
	2963			Clu	Clu	Ean			A na	C15	Lvc			Cln	TIO	C1.0	(Dann)
		,	•	GTA	GLU		1110	мта	ni g	GLY		115	ura	61.11	rre	_	1120
E>	2964				3			T	T	T			C1	mla so	0.00		
	2966	Pne	PLO	Ald			vai	цув	Leu			PLO	GLY	THE			Tre
	2967				_	.125		_			1130	en I		- 1		.1.35	
	2969	Thr	Pro			ren	Pro	гаг			Val	GIN	Pro			Cys	GIN
	2970				1140					1145		_			1150	_	
	2972	Vai			Met	тyr	Asp			Ala	Gln	ASI			G.Lu	Leu	Ala
	2973			155					.160					1165			
	2975			Lys	Gly	Gln			Asn	Va.L	Leu			Glu	Asp	Pro	Asp
	2976		1.70					175					180				
	2978			Lys	Gly			ser	Gly	Gln			Leu	Phe	Pro	Ser	Asn
E>	2979						190					195					200
	2981	Tyr	Va1	Lys	Leu	Thr	Thr	Asp	Met	Asp	Pro	Ser	Gln	Gln	Trp	Cys	Ser
	2982				1	.205				3	L210				1	.215	
	2984	Asp	Leu	His	Leu	Leu	Asp	Met.	Leu	Thr	Pro	Thr	Gl.u	Arg	Lys	Arg	Gln
	2985			1	1.220				1	1225	•			1	1230		
	2987	Gly	Tyr	lle	His	Glu	Leu	lle	Val	Thr	Glu	Glu	Asn	Tyr	Val.	Asn	Asp
	2988	-	-	1235					240					L245			-
	2990	Leu	Gln	Leu	Val.	Thr	Glu	Ile	Phe	Gln	Lys	Pro	Leu	Thr	Glu	ser	Glu
	2991		.250					255					260				
	_	_					-										

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Input Set : A:\Eganl.app
Output Set: N:\CRF3\01112001\I674237.raw

2993 Leu Leu Thr Glu Lys Glu Val Ala Met Ile Phe Val Asn Trp Lys Glu E--> 2994 269 1270 1275 1280 2996 Leu Tle Met Cys Asn Ile Lys Leu Leu Lys Ala Leu Arg Val Arg Lys 2997 1285 1290 1295 2999 Lys Met Ser Gly Glu Lys Met Pro Val Lys Met 11e Gly Asp 11e Leu 3000 1300 1300 3002 Ser Ala Gln Leu Pro His Met Gln Pro Tyr Ile Arq Phe Cys Ser Cys 3003 1315 1320 1325 3005 Gln Leu Asn Cly Ala Ala Leu 11e Gln Gln Lys Thr Asp Glu Ala Pro 3006 -1330 . 1335 -13403008 Asa Phe Lys Glu Phe Val Lys Arg Leu Ala Met Asp Pro Arg Cys Lys
E--> 3009 345 1350 1355 1360 3011 GIV Met Pro Leu Scr Ser Phe Ile Leu Lys Pro Met Gln Arg Val Thr 3012 1365 1370 1375 3014 Arg Tyr Pro Leu Ile Ile Lys Asn Ile Leu Glu Asn Thr Pro Glu Asn 3015 1380 1385 1390 3017 His Pro Asp His Ser His Leu Lys His Ala Leu Glu Lys Ala Glu Glu 3018 1395 1400 1405 3020 Leu Cys Ser Gln Val Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp 3021 1410 1415 1420 3023 Arg Leu Glu Trp Tle Gln Ala His Val Gln Cys Glu Gly Leu Ser Glu
E--> 3024 (425) 1430 1435 1440 3026 din Leu Val Phe Asn Ser Val Thr Asn Cys Leu Cly Pro Arg Lys Phe 3027 1445 1450 1455. 3029 Leu His Ser Gly Lys Leu Tyr Lys Ala Lys Ser Asn Lys Glu Leu Tyr 3030 1460 1465 3032 Gly Phe Leu Phe Asn Asp Phe Leu Leu Thr Gln Ile Thr Lys Pro 3033 1475 1480 1485 3035 Leu Gly Ser Ser Gly Thr Asp Lys Val Phe Ser Pro Lys Ser Asn Leu 3036 1490 1495 1500 3038 Gln Tyr Lys Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu Val Leu Val E--> 3039 509 1510 1515 1520 3041 Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Ile Phe His Ile Ser 3042 1525 1530 1535 3044 His Ile Asp Arg Val Tyr Thr Leu Arg Ala Glu Ser Ile Asn Glu Arg 3045 1540 1545 3047 Thr Ala Trp Val Gln Lys Ile Lys Ala Ala Ser Glu Leu Tyr Ile Glu 3048 \$1555\$ \$1560\$3050 Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Leu Val Arg Ser Gln Arg 3051 -1570 -1575 -15803053 Ala Thr Gly 11e Gly Arg Leu Met Val Asn Val Val Glu Gly 11e Glu E--> 3054 589 1590 1595 3056 Leu Lys Pro Cys Arg Ser His Gly Lys Ser Ash Pro Tyr Cys Glu Val 3057 1605 1610 1615 3059 Thr Met Gly Ser Gln Cys Bis Ile Thr Lys Thr Ile Gln Asp Thr Leu 3060 1620 1630 3062 Asn Pro Lys Trp Asn Ser Asn Cys Gln Phe Phe lle Arg Asp Leu Glu 3063 1635 1640 16453065 Gln Glu Val Leu Cys Ile Thr Val Phe Glu Arg Asp Gln Phe Ser Pro

DATE: 01/11/2001 RAW SEQUENCE LISTING TIME: 17:14:19 PATENT APPLICATION: US/09/674,237

Imput Set : A:\Eganl.app

Output Set: N:\CRF3\01112001\1674237.raw

3068 Asp Asp Phe Leu Gly Arg Thr Glu Ile Arg Val Ala Asp Ile Lys Lys
E--> 3068 669 1670 1675 1680 3071 ASP Gln Gly Ser Lys Gly Pro Val Thr Lys Cys Leu Leu His Glu 3072 1685 1690 1695 3074 Val Pro Thr Gly Glu Ile Val Val Arg Leu Asp Leu Gln Leu Phe Asp 1705 3075 1700 3077 Glu Pro pp 14-16 3717 <210> SEQ ID NO: 27 3718 <211> LENGTH: 1658 3719 <212> TYPE: PRT 3720 <213> ORGANISM: Mus musculus 3723 Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala 3724 1 5 3726 Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu 3727 20 25 30 3729 Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe 3730 35 3732 Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu 3733 50 55 60 3735 Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile 3736 $\,$ 65 $\,$ $\,$ 70 $\,$ 75 $\,$ 80 3738 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gin Leu Pro Val 3739 85 90 95 3741 Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile 3742 100 105 110 3744 Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln 3745 115 120 125 3747 Pro Len Pro Pro Val Ala Pro 1le Ala Thr Pro Leu Ser Ser Ala Thr 3748 130 135 140 3750 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro 3751 145 3753 Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
3754 165 170 175 3756 Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser 3757 180 185 3759 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala 3760 195 200 205 3760 195 200 3762 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala 2762 210 215 3763 210 21.5 3765 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val 3766 225 230 240 3766 225 230 3768 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp 255 3771 Lys Gl7 Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu 3772 260 270 3772 260 3774 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu 280



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3777	Ala		Ile	Asp	Gly	Asp	Gly	Gln	Leu	Lys	Ala	300	GLU	PHE	116	Leu
3778		290					295		1	2 1 a	C1		Pro	Len	Pro	Len
3778 3780		Met	His	Leu	Thr	ASP	мет	FI.1 ct	гаг	HIG	31.5	(J.L.11	110	1.00		320
3781	305				~ 1	310	14-1	Dwo	Dro	Cor		Δησ	Clv	Glv	Lvs	
3783	Thr	Leu	Pro	Pro	Glu	ren	Val	PIO	PIO	330	FILE	era	OTA	0+1	335	5.2
3784					325	er 3	nul		D =10	230	There	Cln.	LMG	Thr		Glu
3784	val.	Asp	Ser	Val	Asn	G.I y	Tnr	Leu	345	ser	LAT	GIII	шуз	350	0.111	020
3787				340				m	343	mlv~	uho	e ba	Agn		Ara	1.98
3789	Glu	Glu	Pro	Gln	Lys	Lys	reu	51.0	val	THE	PHE	GIU	365	шуэ	111 9	11,70
3790			355					360	<i>a</i> 1	7.00	cl.,	Tue		Ara	Gln	Val
3790	Ala		Tyr	Glu	Arg	GIY	ASN	мес	GIU	ьеи	GIU	380	nrg	ura	0111	
3793		370			4.5	~ .	375	a1	x 1 o	C Lu	A ra		Δla	Glo	LVS	Glu
3795		Met	Glu	GLn	GIn	GIN	Arg	GIU	Ald	OTIL	395	uya	niu	01	1510	400
3796	385				3	390		77.	1 00	c1.	Tou	Cln	G1n	Cln	Glo	
3796 3798	Lys	Glu	Glu	Trp	GLu	Arg	газ	GIII	MIG	410	пеа	OIL	Olu	0111	415	
3799					405			f ma	'A ***	410	Clu	T.O.G	Cln	Ara		Leu
3801	Lys	L_IS	Gln		Glu	Len	GIU	Lys	425	пец	Gra	Бүз	GIII	430	0	
3802			_	420	- 1	~ 1 · ·	01	7 20 00	423	Turc	c1n	Tla	Glu		Ara	Glu
3802	Glu	Arg	GIn	Arg	GIU	GLU	Gitu	440	Mrg	Буз	GLU	1.1.0	445	**** 9	200.9	
3805 3807		_	435		er 3		a1	440	Cln	7 22/1	λra	T.611		Tro	G1 u	Ara
3807	Ala		Lys	GIn	GLU	Leu	455	ALG	G 1.11	arg	Aig	460	G.I. W	t.		
3808 3810		450			a	T	400	Cor	Cln	Tue	(thr		Glu	Gln	Glu	Asp
		Arg	Arg	GIn	GLU	470	Leu	5e1	0.11	цуэ	475	211 9	OLG			480
3811 3813	465					4/0	3 20	tria	Luč	car	Len	His	Len	Glu	Leu	Glu
	Lle	Vai	Arg	ren	ser	Ser	ALG	nys	Llys	490	110.0	1125	3,20,00	03.0	495	
3814				er 1	485	1116.0	c l o	Cln	110	Car	- Glv	A:ra	Len	GIn	Asp	Val
3814	Ala	Val	Asn	GIY	ьys	HIS	(3.1.11	GLD	505	عدى د	OL,		2200	510	L	
3817 3819			_	500	a1	mb ~		Lvc	whr	c:Lu	T.e.II	Glu	Val		Asp	LVS
	Gln	He		гãа	(j.Lf1	THI	(5.1.1)	520	J. 11.L	13 1.11	12000	01.4	525			-
3820 3822			515	7' 0.11	clu	Tlo	Mot	Clu	Tle	Lvs	Gln	Leu			Glu	Leu
	GIn			Leu	GEU	116	535	. Gra	1.1.0	11/5	. 02.,	540				
3823 3825		530		G1	7	T ***	TOU	Tlo	TP577	Leu	. Val			Lvs	Gln	Leu
			Tyr	(3 T II	ASII	550	пес	LILE		1500	555			2		560
3826	545	74	C1	7	Tlo	1 970	Aen	Met	Gln	Leu			Thr	Pro	Asp	Ser
		ASI	GTI	Mrd	565	шуг	21.51.	1 110 0	. (121	570)				575	
3829	a1		Com		TOU	uic	T.37.5	. Lvs	Ser			LVS	Glu	Glu	Leu	Cys
		TEG	s ser	580		. 1112	, шу.	,,	585			1		590		
3832	G)	7. **	LOU	700	ch	clr	I.A.	Ast	Ala	Leu	ı Glu	Lys	Glu	Thr	· Ala	Ser
		AI, 9	595		0.10	((3.1.1	ı nee	600	1			•	605	<u> </u>		
3835			277		Mot	Δer	Ser	^ Phe	Asr	Asr	Glr	Leu	Lys	Glu	Leu	Arg
2020		610	k.				611	5				621	, .			
3838		010	i n illisew	. Acr	· mhr	· Gli	Glr	Leo	Al.a	Let	ı Glu	ı Glr	Let	His	Lys	11e
2011	6.25					630)				631)				040
2047	. 02.	, And	, Aer	T.17	; [.e.	i Tave	s Gli	1 11 <i>e</i>	e G1.u	Arc	g Lys	arc	j Lei	ı Gl.o	ı Glr	ılle
2011					6.45	Š				650	J				03.	,
2016	C1.	100	1370	1.v.s	(.e.	i Gli	ı Ası	o Glu	ı Ala	a Ala	a Arc	J Lys	s Ala	ı Lys	Gli	Gly
2047	,			661)				66:)				0/0	,	
2010	l Tur	, G1.	ι Δer	LEI	i Tre	are	a Glu	ı sei	11.6	e Arc	g Lys	s Glu	ı Glu	ı Glu	ı Glu	Lys
3043	, my	, ()1.1	2 2 2 3 1		· ·											

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/674,237

DATE: 01/11/2001 TIME: 17:14:20

Input Set : A:\Eganl.app .
Output Set: N:\CRF3\01112001\1674237.raw

3850			675					680					685		- 2	
3852	Gln	Lys	Arg	Leu	Cln	Glu	G J. u	$\mathbf{L}_{\mathbf{J}}^{G}\mathbf{S}$	Ser	Cln	Asp	ГÀЗ	Thr	Gln	Glu	GJu
3853		690					695					700				
3855	Glu	Arg	ĹУS	Ala	Glu	Ala	Lys	G1n	Ser	Glu	Thr	Ala	Ser	Ala	Leu	Val
3856	705					710					715					720
3858	Asn	Tyr	Arg	Ala	Leu	Tyr	Pro	Phe	Glu	Ala	Arg	Asn	His	Asp	Glu	Met
3859					725					730					735	
3861	ser	Phe	Ser	Ser	Gly	Asp	Tl.e	He	G1.n	Val	Asp	Glu	Lys	Thr	val.	Gly
3862				740					74.5					750		
3864	Glu	Pro	Gly	Trp	Leu	Tyr	Gly	ser	Phe	Gln	Gly	Lys	Phe	Gly	Trp	Phe
3865			755					760					765			
3867	Pro	Cys	Asn	Tvr	Val	Glu	Lys	Val.	Leu	Ser	Ser	Glu	Lys	Ala	Leu	ser
3868		770		- 2			775					780				
3870	Pro	Lvs	Lvs	Ala	Leu	Leu	Pro	Pro	Thr	Val	Ser	Leu	Ser	Ala	Thr	ser
3871	785		2			790					795					800
3873	Thr	Ser	Ser	Gln	Pro	Pro	Ala	Ser	Val	Thr	Asp	Tyr	His	Asu	Val.	ser
3874				0	805					810					815	
.3876	Phe	Ser	Asn	T.eu		Val	Asn	Thr	Thr	grr	Gln	Gln	Lys	Ser	Ala	Phe
3877	THE	OCI	211,711	820					825	1.			•	830		
3879	The	Ara	Thr		Ser	Pro	Glv	Ser	Val	Ser	Pro	Ile	His	Gly	Gln	Glv
3880	111.1	nra	835	* (4.3.	001			840					845	•		
3882	Cln.	ala		Glu	Agn	Len	Tays		Gln	Ala	Leu	Cvs	Ser	Trp	Thr	Ala
3883	(11.11	850	10.1.	010		2.00	855					860		•		
3885	Lare		C1 u	Asn	His	Len		Phe	ser	Lvs	His	Asp	Val	Il.e	Thr	Val
3886		LLYS	Olu	11011	,,,,,	870				-1-	875	•				880
3888	Tan	Glu	Cln.	Gln	Glu		Tro	Trp	Phe	Glv	Glu	Val	His	Gly	Gly	Arg
3889	2.00	014	0.1.11	02.,	885	,	[890					895	
3891	Glv	Tro	Phe	Pro	LVS	Ser	Tvr	Val	Lys	Leu	Tle	Pro	Gly	Asn	G Lu	Va l.
3892	07	1 11 L		900	4				905					910		
3894	Gln	Ara	Glv		Pro	Glu	Ala	Leu	Tyr	Ala	Ala	Val	Thr	Lys	Lys	Pro
3895	0.2.11		915					920	-				925			
3897	Thr	Ser	Thr	Λla	Tvr	Pro	Val.	Thr	ser	Thr	·Ala	Tyr	Pro	Val	Gly	G.l.u
3898		930					935					940				
3900	Asp	ηνr	He	Ala	Leu	Tvr	Ser	Tyr	Ser	Ser	Val	Glu	Pro	G1y	Asp	Leu
3901	945					950					955					960
3903	Thr	Phe	Thr	Glu	Gly	Glu	Glu	Tle	Leu	Val	Thr	Gln	Lys	Asp	Gly	Glu
3904					965					970					975	
3906	Trp	Фтр	Thr	Glv	Ser	Tle	Gly	Glu	Arq	Thr	Gly	11e	Phe	Pro	Ser	Asn
3907				980			-		985		_			990		
3909	Tyr	Val	Arq	Pro	Lvs	Asp	Gln	Glu	Asn	Phe	Gly	Asn	Ala	ser	Lys	ser
391.0	- 1		995		-	•		1000			_		1.005			
3912	Gly	Ala	Ser	Asn	Lvs	Lvs	Pro	Glu	Ile	Ala	G1n	Val	Thr	Ser	Ala	Tyr
3913		1010	D 4.				1015					1.020				
3915			Ser	GIV	Thr			Leu	ser	Leu	Ala	Pro	GLy	Gl n	Leu	Lle
3916	025)				1030					1035					1040
3918	Leu	ile	Leu	Lys	Lys	Asn	Thr	ser	Gly	Trp	Trp	Gln	Gly	Glu	Leu	Gln
3919					1045					1050					1055	
3921	Ala	Arq	Gl.y	Lys	Lys	Arg	Gln	Lys	Gly	Trp	Phe	Pro	Ala	ser	His	Val
3922		_		1.060		-			1065					1070		

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RAW SEQUENCE LISTING DATE: 01/11/2001 TIME: 17:14:20

Input Set : A:\Eganl.app
Output Set: N:\CRF3\01112001\\I674237.raw

3924 Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met Pro Thr Phe His Ala 3927 Val Cys Gln Val Ile Ala Met Tyr Asp Tyr Met Ala Asn Asn Glu Asp 3928 1090 1095 3939 Trp Cys Ala Asp Leu Gln Ala Leu Asp Thr Met Gln Pro Thr Glu Arg
3940 1155 1160 3942 Lys Arg Gln Gly Tyr lle His Glu Leu 1le Gln Thr Glu Glu Arg Tyr 1175 1180 3945 Met Asp Asp Leu Gin Leu Val Ile Glu Val Phe Gin Lys Arg Met
E--> 3946 185 1190 1195 1200 3948 Ala Glu Glu Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val 3948 Ala Glu Glu Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val 3949 1205 1210 3951 Asn Trp Lys Glu Leu Tle Met Ser Asn Thr Lys Leu Leu Arg Ala Leu 1225 1230 3952 1220 1220 1220 1220 1235 3954 Arg Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile 3955 1235 1240 1245 3957 Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile Arg 3958 1250 1255 1260 3960 Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln Lys Thr
1280

E--> 3961 265

3963 Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu Ala Ser Asp
1290

1295

3964

3966 Pro Arg Cys Tyn Gly Mat Pro Los Cor Grap Phe Leu Lys Lys Lys Leu Ala Ser Asp 3966 Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu Leu Lys Pro Met. 1306 1307 1300 3969 Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg Ser Ile Leu Glu Asn 1320 1325 3972 Thr Pro Gln Ser His Val Asp His Ser Ser Leu Lys Leu Ala Leu Glu 3973 1330 1335 3975 Arg Ala Glu Glu Leu Cys Ser Gln Val Asn Glu Gly Val Arg Glu Lys
3975 Arg Ala Glu Glu Leu Cys Ser Gln Val Asn 355
1360 3978 Glu Asn Ser Asp Arg Leu Glu Trp Ile Gln Ala His Val Gln Cys Glu
3979 1365 1370 1375 3981 Gly Leu Ala Glu Gln Leu IIe Phe Asn Ser Leu Thr Asn Cys Leu Gly 3982 1380 1385 3984 Pro Arg Lys Leu His Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn 3985 1395 1400 3987 Lys Glu Leu His Ala Phe Leu Phe Asn Asp Phe Leu Leu Eu Thr Tyr 3988 1410 1415 1420 3990 Len Val Arg Gln Phe Ala Ala Ser Gly His Glu Lys Leu Phe Asn 1440 3993 Ser Lys Ser Ser Ala Gin Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu 3994 1445 1450 3996 Asn Glu Val Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro RAW SEQUENCE LISTING DATE: 01/11/2001
PATENT APPLICATION: US/09/674,237 TIME: 17:14:20

Input Set : A:\Eganl.app
Output Set: N:\CRF3\01112001\1674237.raw

1465 1460 3999 Val Phe His 1le Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp 1485 4000 1475 1480 4002 Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala Ser 4003 1490 1495 15004011 1le Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn 4012 1540 1545 1550 4012 1540 4014 Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr 4015 \$1555\$ \$1560\$ \$15654017 Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe 4018 1570 1575 15804018 1570 1575 4020 Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg
E--> 4021 (585) 1590 1595 1600 4023 Asp Gin Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val 4024 1605 1610 16154026 Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg 4027 1620 1625 1630 4029 Leu Leu Leu His Glu Val Pro Thr Gly Glu Val Trp Val Arg Phe Asp 4030. 1635 1640 1645 4032 Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu 4033 1650

> sel following page for more errors

<210> 18							
<211> 1521							
<212> DNA							
□ <213> Mus m	usculus						
□ <400> 18							
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□ ctggagcaac □	tgcgcaccga	ggtggatgtg	cgcattagcg	onntggacac	ctgcgtcaag	120	Jen 10
□ gccaagtcgc □	tgccagccgt	cccgccgaga	gtctcaggcc	cacccccgaa	ccctccaccc	180	Jen 10 on Ever Jumary Sheet
□ attgatccag □	ctagcctgga	ggaattcaag	aaaaggatcc	tggagtctca	geggeteeet	240	Sheet
□ gtagtcaacc □	ctgcwgccca	acccagcggt	tgagraccca	gctgccgcag	gacgctgggt	300	
□ gccagaatcg □	cccacctgtg	gatgggggca	gccaggtgcc	cacagtgctg	gacacccgcc	360	
□ gtgcctgccg □	gcagcctcca	ccccagcgc	cttctctggc	accccttcac	tgtcccstgc	420	
□ atccccrcca □	ttcsscasws	askggattta	aggcacacac	agctgtgaga	tgacttcaca	480	
□ tcgacccctt □	gtgcagtgac	ccggatggtg	cccacccac	acatgaagca	cccacagctc	540	
agctgccacc	ctaggcaact	cctccggttt	cctatcactc	tgctcctgac	ccgggaggtg	600	
□ agaacaggaa □	gcccagcctt	cagctccctt	gggagtttcc	agcctccctc	ttaaaggcca	660	
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only enoug portion of Sequence 18 show

VERIFICATION SUMMARY

M:332 Repeated in SeqNo=27

PATENT APPLICATION: US/09/674,237

DATE: 01/11/2001 TIME: 17:14:21

Input Set : A:\Eganl.app

Output Set: N:\CRF3\01112001\1674237.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:711 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 M:332 Repeated in SeqNo=3 L:1421 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 M:332 Repeated in SeqNo=6 L:1979 M:258 W: Mandatory Feature missing, 220> not found for SEQ ID:18 L:1979 M:258 W: Mandatory Feature missing, 222> not found for SEQ ID:18 L:1979 M:258 W: Mandatory Feature missing, 222> not found for SEQ ID:18 L:1979 M:258 W: Mandatory Feature missing, 222> not found for SEQ ID:18 L:1979 M:258 W: Mandatory Feature missing, 223> not found for SEQ ID:18 L:1979 M:330 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID:18 L:2747 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23 L:2949 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24 M:332 Repeated in SeqNo=24 L:3916 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27